IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Rachel A. Meyers
Serial No. : Unassigned
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Title : 33521, A NOVEL HUMAN GUANINE NUCLEOTIDE EXCHANGE FAMILY MEMBER AND USES THEREOF

BOX PATENT APPLICATION
Commissioner for Patents
Washington, D.C. 20231

VERIFIED STATEMENT UNDER 37 CFR §1.821(f)

I, Katica Magovcevic, declare that I personally prepared the paper and the computer-readable copy of the Sequence Listing filed herewith for the above-identified application and that the content of both is the same.

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of The United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 9/24/01

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JOANNE D. BOYLE
Typed or Printed Name of Person Signing Certificate

SEQUENCE LISTING

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Val Asp Gly Val Pro Arg Asp Asn Ala Trp Glu Ile Gln Thr Tyr Val
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His Phe Gln Asp Asn His Gly Val Thr Val Gly Ile Lys Pro Glu His
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aga gta gaa gat att ttg act ttg gca tgc aag atg agg cag ttg gaa      2785
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Pro Ser His Tyr Gly Leu Gln Leu Arg Lys Leu Val Asp Asp Asn Val
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Asp Gly Leu Ala Tyr Gly Glu Gly Leu Arg Lys Gly Asn Glu Ile Met
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acc tta aat ggg gaa gct gtg tct gat ctt gac ctt aag cag atg gag      3121
Thr Leu Asn Gly Glu Ala Val Ser Asp Leu Asp Leu Lys Gln Met Glu
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gcc ctg ttt tct gag aag agc gtc gga ctc act ctg att gcc cgg cct      3169
Ala Leu Phe Ser Glu Lys Ser Val Gly Leu Thr Leu Ile Ala Arg Pro
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ccg gac aca aaa gca acc ctg tgt aca tcc tgg tca gac agt gac ctg      3217
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Asp Gly Thr Leu Asp Gln Val Ser His Arg Glu Lys Met Glu Gln Thr
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Ser Gln Ala Asn Gly Met Glu Gly Pro Arg Glu Asn Gln Asp Pro Pro
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Lys Leu Tyr Ser Gly Phe Cys Ala Asn His Ile Lys Val Gln Lys Val
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ctg gag cga gct aaa act gac aaa gcc ttc aag gct ttt ctg gat gcc      3937
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Val Ser Leu Thr Asp Gln Glu Ser Glu Glu His Tyr His Leu Thr Glu
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ctg atg cac tct acg gtt tcc tgg ttg aat cca ttt ctg tct cta gga     4273
Leu Met His Ser Thr Val Ser Trp Leu Asn Pro Phe Leu Ser Leu Gly
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aaa gct aga aag gac ctt gag ctc aca gta ttt gtt ttt aag aga gcc     4321
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Val Ile Leu Val Tyr Lys Glu Asn Cys Lys Leu Lys Lys Lys Leu Pro
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Phe Arg Trp Leu Ile Pro Ile Ser Ala Leu Gln Val Arg Leu Gly Asn
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cca gca ggg aca gaa aat aat tcc ata tgg gaa ctg atc cat acg aag     4513
Pro Ala Gly Thr Glu Asn Asn Ser Ile Trp Glu Leu Ile His Thr Lys
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Ser Glu Ile Glu Gly Arg Pro Glu Thr Ile Phe Gln Leu Cys Cys Ser
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Ala Lys Leu Ala Ser Ser Arg Ser Leu Lys Val Leu Lys Asn Ser Ser
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Ile Leu Ser Asp Glu Asp Asp Asp His Arg Gln Thr Val Lys Gln Gly
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65                  70                  75                  80
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Asn Ala Pro Gly Lys Asp Phe Gln Gly Ile Ser Ala Ala Phe Ser Thr
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Glu Asn Gly Phe His Ser Val Gly His Glu Leu Ala Asp Asn His Ile
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Thr Ser Arg Asp Cys Asn Gly His Leu Leu Asn Cys Tyr Gly Arg Asn
    130                 135                 140
Glu Ser Ile Ala Ser Thr Pro Pro Gly Glu Asp Arg Lys Ser Pro Arg
145                 150                 155                 160
Val Leu Ile Lys Thr Leu Gly Lys Pro Asp Gly Cys Leu Arg Val Glu
                165                 170                 175
Phe His Asn Gly Gly Asn Pro Ser Lys Val Pro Ala Glu Asp Cys Ser
            180                 185                 190
Glu Pro Val Gln Leu Leu Arg Tyr Ser Pro Thr Leu Ala Ser Glu Thr
        195                 200                 205
Ser Pro Val Pro Glu Ala Arg Arg Gly Ser Ser Ala Asp Ser Leu Pro
    210                 215                 220
Ser His Arg Pro Ser Pro Thr Asp Ser Arg Leu Arg Ser Ser Lys Gly
225                 230                 235                 240
Ser Ser Leu Ser Ser Glu Ser Ser Trp Tyr Asp Ser Pro Trp Gly Asn
                245                 250                 255
Ala Gly Glu Leu Ser Glu Ala Glu Gly Ser Phe Leu Ala Pro Gly Met
            260                 265                 270
Pro Asp Pro Ser Leu His Ala Ser Phe Pro Pro Gly Asp Ala Lys Lys
        275                 280                 285
Pro Phe Asn Gln Ser Ser Ser Leu Ser Ser Leu Arg Glu Leu Tyr Lys
    290                 295                 300
Asp Ala Asn Leu Gly Ser Leu Ser Pro Ser Gly Ile Arg Leu Ser Asp
305                 310                 315                 320
Glu Tyr Met Gly Thr His Ala Ser Leu Ser Asn Arg Val Ser Phe Ala
                325                 330                 335
Ser Asp Ile Asp Val Pro Ser Arg Val Ala His Gly Asp Pro Ile Gln
            340                 345                 350
Tyr Ser Ser Phe Thr Leu Pro Cys Arg Lys Pro Lys Ala Phe Val Glu
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        355                 360                 365
Asp Thr Ala Lys Lys Asp Ser Leu Lys Ala Arg Met Arg Arg Ile Ser
    370                 375                 380
Asp Trp Thr Gly Ser Leu Ser Arg Lys Lys Arg Lys Leu Gln Glu Pro
385                 390                 395                 400
Arg Ser Lys Glu Gly Ser Asp Tyr Phe Asp Ser Arg Ser Asp Gly Leu
                405                 410                 415
Asn Thr Asp Val Gln Gly Ser Ser Gln Ala Ser Ala Phe Leu Trp Ser
            420                 425                 430
Gly Gly Ser Thr Gln Ile Leu Ser Gln Arg Ser Glu Ser Thr His Ala
        435                 440                 445
Ile Gly Ser Asp Pro Leu Arg Gln Asn Ile Tyr Glu Asn Phe Met Arg
    450                 455                 460
Glu Leu Glu Met Ser Arg Thr Asn Thr Glu Asn Ile Glu Thr Ser Thr
465                 470                 475                 480
Glu Thr Ala Glu Ser Ser Ser Glu Ser Leu Ser Ser Leu Glu Gln Leu
                485                 490                 495
Asp Leu Leu Phe Glu Lys Glu Gln Gly Val Val Arg Arg Ala Gly Trp
            500                 505                 510
Leu Phe Phe Lys Pro Leu Val Thr Val Gln Lys Glu Arg Lys Leu Glu
        515                 520                 525
Leu Val Ala Arg Arg Lys Trp Lys Gln Tyr Trp Val Thr Leu Lys Gly
    530                 535                 540
Cys Thr Leu Leu Phe Tyr Glu Thr Tyr Gly Lys Asn Ser Met Asp Gln
545                 550                 555                 560
Ser Ser Ala Pro Arg Cys Ala Leu Phe Ala Glu Asp Ser Ile Val Gln
                565                 570                 575
Ser Val Pro Glu His Pro Lys Lys Glu Asn Val Phe Cys Leu Ser Asn
            580                 585                 590
Ser Phe Gly Asp Val Tyr Leu Phe Gln Ala Thr Ser Gln Thr Asp Leu
        595                 600                 605
Glu Asn Trp Val Thr Ala Val His Ser Ala Cys Ala Ser Leu Phe Ala
    610                 615                 620
Lys Lys His Gly Lys Glu Asp Thr Leu Arg Leu Leu Lys Asn Gln Thr
625                 630                 635                 640
Lys Asn Leu Leu Gln Lys Ile Asp Met Asp Ser Lys Met Lys Lys Met
                645                 650                 655
Ala Glu Leu Gln Leu Ser Val Val Ser Asp Pro Lys Asn Arg Lys Ala
            660                 665                 670
Ile Glu Asn Gln Ile Gln Gln Trp Glu Gln Asn Leu Glu Lys Phe His
        675                 680                 685
Met Asp Leu Phe Arg Met Arg Cys Tyr Leu Ala Ser Leu Gln Gly Gly
    690                 695                 700
Glu Leu Pro Asn Pro Lys Ser Leu Leu Ala Ala Ala Ser Arg Pro Ser
705                 710                 715                 720
Lys Leu Ala Leu Gly Arg Leu Gly Ile Leu Ser Val Ser Ser Phe His
                725                 730                 735
Ala Leu Val Cys Ser Arg Asp Asp Ser Ala Leu Arg Lys Arg Thr Leu
            740                 745                 750
Ser Leu Thr Gln Arg Gly Arg Asn Lys Lys Gly Ile Phe Ser Ser Leu
        755                 760                 765
Lys Gly Leu Asp Thr Leu Ala Arg Lys Gly Lys Glu Lys Arg Pro Ser
    770                 775                 780
Ile Thr Gln Val Asp Glu Leu Leu His Ile Tyr Gly Ser Thr Val Asp
785                 790                 795                 800
Gly Val Pro Arg Asp Asn Ala Trp Glu Ile Gln Thr Tyr Val His Phe
                805                 810                 815
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Gln Asp Asn His Gly Val Thr Val Gly Ile Lys Pro Glu His Arg Val
820 825 830
Glu Asp Ile Leu Thr Leu Ala Cys Lys Met Arg Gln Leu Glu Pro Ser
835 840 845
His Tyr Gly Leu Gln Leu Arg Lys Leu Val Asp Asp Asn Val Glu Tyr
850 855 860
Cys Ile Pro Ala Pro Tyr Glu Tyr Met Gln Gln Gln Val Tyr Asp Glu
865 870 875 880
Ile Glu Val Phe Pro Leu Asn Val Tyr Asp Val Gln Leu Thr Lys Thr
885 890 895
Gly Ser Val Cys Asp Phe Gly Phe Ala Val Thr Ala Gln Val Asp Glu
900 905 910
Arg Gln His Leu Ser Arg Ile Phe Ile Ser Asp Val Leu Pro Asp Gly
915 920 925
Leu Ala Tyr Gly Glu Gly Leu Arg Lys Gly Asn Glu Ile Met Thr Leu
930 935 940
Asn Gly Glu Ala Val Ser Asp Leu Asp Leu Lys Gln Met Glu Ala Leu
945 950 955 960
Phe Ser Glu Lys Ser Val Gly Leu Thr Leu Ile Ala Arg Pro Pro Asp
965 970 975
Thr Lys Ala Thr Leu Cys Thr Ser Trp Ser Asp Ser Asp Leu Phe Ser
980 985 990
Arg Asp Gln Lys Ser Leu Leu Pro Pro Pro Asn Gln Ser Gln Leu Leu
995 1000 1005
Glu Glu Phe Leu Asp Asn Phe Lys Lys Asn Thr Ala Asn Asp Phe Ser
1010 1015 1020
Asn Val Pro Asp Ile Thr Thr Gly Leu Lys Arg Ser Gln Thr Asp Gly
1025 1030 1035 1040
Thr Leu Asp Gln Val Ser His Arg Glu Lys Met Glu Gln Thr Phe Arg
1045 1050 1055
Ser Ala Glu Gln Ile Thr Ala Leu Cys Arg Ser Phe Asn Asp Ser Gln
1060 1065 1070
Ala Asn Gly Met Glu Gly Pro Arg Glu Asn Gln Asp Pro Pro Pro Arg
1075 1080 1085
Pro Leu Ala Arg His Leu Ser Asp Ala Asp Arg Leu Arg Lys Val Ile
1090 1095 1100
Gln Glu Leu Val Asp Thr Glu Lys Ser Tyr Val Lys Asp Leu Ser Cys
1105 1110 1115 1120
Leu Phe Glu Leu Tyr Leu Glu Pro Leu Gln Asn Glu Thr Phe Leu Thr
1125 1130 1135
Gln Asp Glu Met Glu Ser Leu Phe Gly Ser Leu Pro Glu Met Leu Glu
1140 1145 1150
Phe Gln Lys Val Phe Leu Glu Thr Leu Glu Asp Gly Ile Ser Ala Ser
1155 1160 1165
Ser Asp Phe Asn Thr Leu Glu Thr Pro Ser Gln Phe Arg Lys Leu Leu
1170 1175 1180
Phe Ser Leu Gly Gly Ser Phe Leu Tyr Tyr Ala Asp His Phe Lys Leu
1185 1190 1195 1200
Tyr Ser Gly Phe Cys Ala Asn His Ile Lys Val Gln Lys Val Leu Glu
1205 1210 1215
Arg Ala Lys Thr Asp Lys Ala Phe Lys Ala Phe Leu Asp Ala Arg Asn
1220 1225 1230
Pro Thr Lys Gln His Ser Ser Thr Leu Glu Ser Tyr Leu Ile Lys Pro
1235 1240 1245
Val Gln Arg Val Leu Lys Tyr Pro Leu Leu Leu Lys Glu Leu Val Ser
1250 1255 1260
Leu Thr Asp Gln Glu Ser Glu Glu His Tyr His Leu Thr Glu Ala Leu

```
1265                1270                1275                1280
Lys Ala Met Glu Lys Val Ala Ser His Ile Asn Glu Met Gln Lys Ile
                1285                1290                1295
Tyr Glu Asp Tyr Gly Thr Val Phe Asp Gln Leu Val Ala Glu Gln Ser
            1300                1305                1310
Gly Thr Glu Lys Glu Val Thr Glu Leu Ser Met Gly Glu Leu Leu Met
        1315                1320                1325
His Ser Thr Val Ser Trp Leu Asn Pro Phe Leu Ser Leu Gly Lys Ala
    1330                1335                1340
Arg Lys Asp Leu Glu Leu Thr Val Phe Val Phe Lys Arg Ala Val Ile
1345                1350                1355                1360
Leu Val Tyr Lys Glu Asn Cys Lys Leu Lys Lys Lys Leu Pro Ser Asn
                1365                1370                1375
Ser Arg Pro Ala His Asn Ser Thr Asp Leu Asp Pro Phe Lys Phe Arg
            1380                1385                1390
Trp Leu Ile Pro Ile Ser Ala Leu Gln Val Arg Leu Gly Asn Pro Ala
        1395                1400                1405
Gly Thr Glu Asn Asn Ser Ile Trp Glu Leu Ile His Thr Lys Ser Glu
    1410                1415                1420
Ile Glu Gly Arg Pro Glu Thr Ile Phe Gln Leu Cys Cys Ser Asp Ser
1425                1430                1435                1440
Glu Ser Lys Thr Asn Ile Val Lys Val Ile Arg Ser Ile Leu Arg Glu
                1445                1450                1455
Asn Phe Arg Arg His Ile Lys Cys Glu Leu Pro Leu Glu Lys Thr Cys
            1460                1465                1470
Lys Asp Arg Leu Val Pro Leu Lys Asn Arg Val Pro Val Ser Ala Lys
        1475                1480                1485
Leu Ala Ser Ser Arg Ser Leu Lys Val Leu Lys Asn Ser Ser Ser Asn
    1490                1495                1500
Glu Trp Thr Gly Glu Thr Gly Lys Gly Thr Leu Leu Asp Ser Asp Glu
1505                1510                1515                1520
Gly Ser Leu Ser Ser Gly Thr Gln Ser Ser Gly Cys Pro Thr Ala Glu
                1525                1530                1535
Gly Arg Gln Asp Ser Lys Ser Thr Ser Pro Gly Lys Tyr Pro His Pro
            1540                1545                1550
Gly Leu Ala Asp Phe Ala Asp Asn Leu Ile Lys Glu Ser Asp Ile Leu
        1555                1560                1565
Ser Asp Glu Asp Asp Asp His Arg Gln Thr Val Lys Gln Gly Ser Pro
    1570                1575                1580
Thr Lys Asp Ile Glu Ile Gln Phe Gln Arg Leu Arg Ile Ser Glu Asp
1585                1590                1595                1600
Pro Asp Val His Pro Glu Ala Glu Gln Gln Pro Gly Pro Glu Ser Gly
                1605                1610                1615
Glu Gly Gln Lys Gly Gly Glu Gln Pro Lys Leu Val Arg Gly His Phe
            1620                1625                1630
Cys Pro Ile Lys Arg Lys Ala Asn Ser Thr Lys Arg Asp Arg Gly Thr
        1635                1640                1645
Leu Leu Lys Ala Gln Ile Arg His Gln Ser Leu Asp Ser Gln Ser Glu
    1650                1655                1660
Asn Ala Thr Ile Asp Leu Asn Ser Val Leu Glu Arg Glu Phe Ser Val
1665                1670                1675                1680
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Ser His Gly Lys Ser
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<211> 5106
<212> DNA
<213> Homo sapiens

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aagtcattgc atggatgggg tcacgggagc aacggagcag gttacaagtc caggtccctg 180
gcccgaagct gcctttctca ctttaagagt aaccagcctt acgcatcgag actcggtggc 240
cccacatgca aggtctccag aggtgttgcc tactccacgc acaggacaaa tgccccaggg 300
aaggatttcc agggcatcag tgctgctttc tcaactgaga atggcttcca ttctgttggc 360
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tacgggagga atgagagcat tgcctccacc ccaccgggcg aagaccgcaa gagcccccga 480
gtgctcatca aaacgctggg gaagccggat gggtgtttaa gggtcgagtt ccacaatggt 540
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<210> 4
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 4

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Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Lys Ser Trp Lys Lys
 1               5                  10                  15
Arg Tyr Phe Val Leu Phe Asn Asn Val Leu Leu Tyr Tyr Lys Asp Ser
            20                  25                  30
Lys Lys Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Gln Val Glu
        35                  40                  45
Lys Pro Asp Lys Asn Cys Phe Glu Ile Arg Thr Asp Arg Thr Leu Leu
    50                  55                  60
Leu Gln Ala Glu Ser Glu Glu Glu Arg Lys Glu Trp Val Lys Ala Ile
65                  70                  75                  80
Gln Ser Ala Ile Arg
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85

<210> 5
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 5
Lys Thr Ile Arg Val His Leu Pro Asn Asn Gln Arg Ser Val Val Glu
1 5 10 15
Val Arg Pro Gly Met Thr Val Arg Asp Ala Leu Ala Lys Ala Leu Lys
20 25 30
Lys Arg Gly Leu Asn Pro Ser Ala Cys Val Val Arg Arg Ser Gly Asp
35 40 45
Pro Gln Glu Gly Glu Lys Lys Pro Leu Asp Leu Asp Thr Asp Ile Ser
50 55 60
Ser Leu Pro Gly Pro Glu Glu Leu Val Val Glu Asn Leu
65 70 75

<210> 6
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 6
Glu Ile Thr Leu Glu Lys Glu Val Lys Arg Gly Gly Leu Gly Phe Ser
1 5 10 15
Ile Lys Gly Gly Ser Asp Lys Gly Ile Val Val Ser Glu Val Leu Pro
20 25 30
Gly Ser Gly Ala Ala Glu Ala Gly Gly Arg Leu Lys Glu Gly Asp Val
35 40 45
Ile Leu Ser Val Asn Gly Gln Asp Val Glu Asn Met Ser His Glu Arg
50 55 60
Ala Val Leu Ala Ile Lys Gly Ser Gly Gly Glu Val Thr Leu Thr Val
65 70 75 80
Leu Arg Asp

<210> 7
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 7
Val Leu Lys Glu Leu Leu Glu Thr Glu Lys Lys Tyr Val Arg Asp Leu
1 5 10 15
Glu Ile Leu Asp Asn Val Tyr Met Lys Pro Leu Arg Glu Ala Ala Ile
20 25 30

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Ser Ser Lys Pro Val Leu Thr Pro Asp Asp Ile Glu Thr Ile Phe Ser
        35                  40                  45
Asn Ile Glu Asp Ile Tyr Glu Phe His Arg Glu Phe Leu Lys Ser Ser
    50                  55                  60
Leu Glu Ala Arg Ile Ser Ser Ser Gln Phe Glu Asp Leu Asp Glu Lys
65                  70                  75                  80
Lys Ile Glu Pro Ser Ala Pro Arg Leu Gly Asp Leu Phe Leu Lys Leu
                85                  90                  95
Lys Glu Pro Phe Leu Gln Val Tyr Gly Glu Tyr Cys Ser Asn Lys Pro
            100                 105                 110
Tyr Ala Gln Glu Leu Leu Glu Lys Leu Arg Gln Ala Ala Ser Asn Pro
        115                 120                 125
Gln Phe Ala Glu Phe Leu Asp Glu Val Glu Ala Ser Ser Asn Thr Gly
    130                 135                 140
Ala Lys Asp Asp Ala Val Lys Leu Thr Leu Gln Ser Leu Leu Leu Lys
145                 150                 155                 160
Pro Val Gln Arg Ile Leu Arg Tyr Pro Leu Leu Leu Lys Glu Leu Leu
                165                 170                 175
Lys His Thr Pro Glu Gly Glu Asp Gln Pro Asp Arg Glu Asp Leu Lys
            180                 185                 190
Lys Ala Leu Asp Leu Leu Gln Asp Leu Ala Lys Ser Ile Asn Glu
        195                 200                 205

<210> 8
<211> 67
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 8
Phe Val Leu Phe Asn Asn Val Leu Leu Tyr Tyr Lys Asp Ser Lys Lys
 1               5                  10                  15
Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Gln Val Glu Lys Pro
            20                  25                  30
Asp Lys Asn Cys Phe Glu Ile Arg Thr Asp Arg Thr Leu Leu Leu Gln
        35                  40                  45
Ala Glu Ser Glu Glu Glu Arg Lys Glu Trp Val Lys Ala Ile Gln Ser
    50                  55                  60
Ala Ile Arg
65

<210> 9
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 9
Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Lys Ser Trp Lys Lys
 1               5                  10                  15
Arg Tyr Phe Val Leu Phe Asn Gly Val Leu Leu Tyr Tyr Lys Ser Lys
            20                  25                  30
Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Ser Val Arg Glu Pro
```

```
        35                  40                  45
Cys Phe Glu Ile Val Thr Asp Arg Thr Leu Leu Leu Gln Ala Glu Ser
    50                  55                  60
Glu Glu Glu Arg Glu Glu Trp Val Glu Ala Leu Gln Ser Ala Ile Ala
65                  70                  75                  80
Lys Ala
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<210> 10
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 10

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Lys Thr Cys Arg Val His Leu Pro Asp Asn Gln Arg Thr Val Val Lys
 1               5                  10                  15
Val Arg Pro Gly Lys Thr Val Arg Asp Ala Leu Ala Lys Ala Leu Lys
            20                  25                  30
Lys Arg Gly Leu Asn Pro Glu Ala Cys Val Val Arg Leu Arg Gly Asp
        35                  40                  45
Pro Gln Glu Gly Glu Lys Lys Pro Leu Asp Leu Asn Gln Asp Ile Ser
    50                  55                  60
Ser Leu Ala Gly Gln Glu Leu Val Val Glu Glu Leu
65                  70                  75
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<210> 11
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 11

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Gly Gly Leu Gly Phe Ser Ile Val Gly Gly Ile Phe Val Ser Ser Val
 1               5                  10                  15
Val Pro Gly Ser Pro Ala Ala Lys Ala Gly Arg Lys Ser Leu Gly Leu
            20                  25                  30
Leu Lys Val Gly Asp Val Ile Leu Glu Val Asn Gly Glu Thr Ser Val
        35                  40                  45
Glu Gly Leu Thr His Glu Glu Ala Val Asp Leu Leu Lys Lys Ala Gly
    50                  55                  60
Gly Gly Gly Val Gly Glu Lys Val Thr Leu Thr Val Leu Arg Gly Gly
65                  70                  75                  80
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<210> 12
<211> 211
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 12

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Val Leu Lys Glu Leu Leu Gln Thr Glu Arg Asn Tyr Val Arg Asp Leu
 1               5                  10                  15
Lys Ile Leu Val Glu Val Phe Leu Lys Pro Leu Lys Lys Glu Ala Lys
            20                  25                  30
Ser Ser Leu Leu Pro Leu Leu Ser Pro Asp Glu Val Lys Thr Leu Phe
        35                  40                  45
Gly Pro Asn Ile Glu Glu Ile Tyr Glu Phe His Arg Arg Phe Leu Asp
    50                  55                  60
Glu Leu Glu Glu Arg Val Glu Glu Trp Leu Leu Ser Lys Asp Leu Lys
65                  70                  75                  80
Ser Glu Arg Asn Ser Val Ile Glu Asp Ser Gly Glu Arg Ile Gly Asp
                85                  90                  95
Val Phe Leu Lys Leu Phe Ser Ala Glu Glu Phe Phe Lys Ile Tyr Ser
            100                 105                 110
Glu Tyr Cys Ser Asn His Pro Asp Ala Leu Glu Leu Leu Lys Lys Leu
        115                 120                 125
Met Lys Lys Lys Lys Asn Pro Ala Phe Gln Lys Phe Leu Lys Glu Ile
    130                 135                 140
Glu Ser Lys Pro Asn Cys Arg Ser Lys Ser Glu Ala Arg Leu Thr Leu
145                 150                 155                 160
Glu Ser Leu Leu Ile Lys Pro Val Gln Arg Leu Thr Lys Tyr Pro Leu
                165                 170                 175
Leu Leu Lys Glu Leu Leu Lys His Thr Pro Pro Asp His Glu Asp Arg
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Val Asn Glu
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            20                  25                  30
Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Ser Val Arg Glu Pro
        35                  40                  45
Cys Phe Glu Ile Val Thr Asp Arg Thr Leu Leu Leu Gln Ala Glu Ser
    50                  55                  60
Glu Glu Glu Arg Glu Glu Trp Val Glu Ala Leu Gln Ser Ala Ile Ala
65                  70                  75                  80
Lys Ala
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